

LITERATURE REVIEWS

By John Brittnacher

Furches, M.S., Small, R.L., and Furches, A. 2013. Genetic diversity in three endangered pitcher plant species (*Sarracenia*; Sarraceniaceae) is lower than widespread congeners. *American Journal of Botany* 100(10): 2092-2101.

The U.S. Fish & Wildlife Service lists *Sarracenia alabamensis*, *S. oreophila*, and *S. jonesii* as endangered species. To determine the genetic diversity or genetic health within these species this study sampled between 4-15 clumps (*i.e.* presumed individuals) from 3 of the about 6 *S. alabamensis* sites known, 8 of the 40 *S. oreophila* sites, and 6 of the 10 *S. jonesii* sites. The number of clumps per site varied as half the sites had very few plants. The *S. alabamensis* sites had 8 to 12 clumps of plants each, 3 of the *S. oreophila* sites had 5 to 11 clumps, and 3 of the *S. jonesii* sites had 4 to 6 clumps. The authors determined chloroplast non-coding DNA sequences and DNA microsatellite data from small leaf samples. (Non-coding DNA sequences and the small tandem repeat DNA sequences that constitute the “microsatellites” evolve very quickly. The microsatellite procedure consists of assessing the size of selected microsatellites and not their actual DNA sequences.) For the chloroplast DNA sequences recovered in the study, each of the species had a unique set of variants. There was no variation within the *S. jonesii* plants while there were two variants within *S. alabamensis*. The North Carolina and Georgia *S. oreophila* sites near Lake Chatuge had the same unique variant while the Alabama sites had 13 variants including one site with 6 variants. On the other hand, *S. alabamensis* was found to have the highest level of microsatellite variation although at the two smaller sites there was significant inbreeding measured. *S. oreophila* had the lowest microsatellite variation and significant inbreeding at half the sites. *S. jonesii* had intermediate microsatellite variation and significant inbreeding at 2 of 6 sites. Comparing their genetic data and their field observations, the authors conclude that the current conservation status of a species is not a predictor of their current genetic status. Although this is true, they did not consider that high inbreeding coefficients indicate the current populations are too small to maintain the amount of variation they measured. Among these species, *S. alabamensis* is the most threatened owing to it being present only in a few small sites, many of them threatened with degradation. *S. oreophila* is in somewhat better shape because there are more sites but those sites are equally threatened. *S. jonesii* is much less likely to become extinct in its native sites because they are within a state park, wilderness area, or private reserve.

Furches, M.S., Small, R.L., and Furches, A. 2013. Hybridization leads to interspecific gene flow in *Sarracenia* (Sarraceniaceae). *American Journal of Botany* 100(10): 2085-2091.

The genus *Sarracenia* consists of 15 species and subspecies, all of which are capable of hybridizing. There are many locations where two or more *Sarracenia* species coexist and hybrids are found. This study addresses the question of whether effective gene flow is occurring between the species where they coexist. It used microsatellite DNA because microsatellite analysis is a relatively inexpensive and easy way to characterize a large number of samples within species and between very closely related species. The authors analyzed 292 plants sampled randomly from a site in Washington County, Alabama, that has *Sarracenia leucophylla*, *S. alata*, and *S. rubra* subsp. *wherryi*. As controls they sampled 5, 9, and 6 individuals from those species respectively from sites 250 km, 80 km, and 15 km away respectively that only had that one species. Their results showed no individuals at the multispecies site as “pure” as at the single species control sites. This makes sense because they could not know whether the sample of microsatellites at the control sites were fully indicative of the whole species.

They would have needed to do a full species survey of microsatellites for better control data. They used 85% or higher “pure” as a cutoff for pure species in the multispecies site in order to not overestimate the proportion of hybrids. They used 40 to 60% each of two species and less than 20% of the third to classify first generation hybrids. The remaining plants were classified as backcross or complex hybrids based on the microsatellite percentages from three species. Using these classifications they found 63% of the plants were pure species, 13% were first generation hybrids, 19% were backcross hybrids, and 5% were complex hybrids. They did not address the issue of how a taxonomist would have classified the plants in each category, although they appear to have had the data to do so. The results indicate that gene flow can and does happen between *Sarracenia* species under natural conditions. The implication of this work is that management strategies for conservation of wild mixed species *Sarracenia* sites must take into account factors that have been shown to increase hybridization.

Carstens, B.C., and Satler, J.D. 2013. The carnivorous plant described as *Sarracenia alata* contains two cryptic species. *Biological Journal of the Linnean Society* 109: 737–746.

This paper addresses the issue of whether it is time for genetic data to be used for taxonomic classification in cases where there are no physical characters to distinguish “species”. It uses DNA sequence data from Zellmer *et al.* (2012) along with new data filling in missing data from the earlier study in order to make the results more robust. This study, like the previous study, is a *tour de force* of cutting edge analysis techniques and is important as a demonstration of their use. However, it has the same major flaw as the previous paper. They assume the eastern population of *Sarracenia alata* is genetically isolated from the four *Sarracenia* species with which it co-occurs. Many authors have noted that interspecific hybrids are found in the eastern *S. alata* populations, making introgression between species possible. As reviewed above, Furches *et al.* (2013) studied a population of three *Sarracenia* species, including eastern *S. alata*, and showed that hybridization appears to have resulted in gene flow between species. In order for the conclusions in this paper to be valid they have to show the differences they found between the eastern and western populations of *S. alata* are based on genetic variants unique to *S. alata* and not a result of introgression from other species. The authors promise a species description to be published based on purely genetic data providing a name for the western population of *S. alata*.

References

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- Zellmer, A.J., Hanes, M.M., Hird, S.M., and Carstens, B.C. 2012. Deep phylogeographic structure and environmental differentiation in the carnivorous plant *Sarracenia alata*. *Syst. Biol.* 61(5): 763-777.

